

SEQUENCE LISTING



<110> AGUERA et al.

<120> Use of ULIP proteins in the diagnosis and therapy of cancers and paraneoplastic neurological syndromes

<130> P06473US0/BAS

<140> US 09/367,496

<141> 1999-11-24

<150> FR 97 01 961

<151> 1997-02-19

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<170> PatentIn version 3.2

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gtacgtcacc aaggtgatga gcaagggggc ggccgacgcc atcgctcagg ccaagcgcag 840
aggggtggtc gtgtttgggg agcccatcac cgccagcctg ggcaccgacg gttcacacta 900
ctggagcaag aactgggcca aggotgcagc cttcgtcaca tccccctg tcaaccaga 960
ccccaccag gcagaccacc tcacctgctt gctgtccagc ggggacctcc aggtgacagg 1020

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cagcgccac tgcaccttca ccactgccca gaaggctgtg ggcaaggaca acttcgcgct 1080
gatccccgag ggcaccaacg gcattgagga gcgcatgtcg atgggtctggg agaaatgtgt 1140
ggcctctggg aagatggacg agaatgagtt cgtcgcggtg accagtacaa atgctgccaa 1200
aatcttcaat ttttacccaa ggaaggggag agtggctgtg ggctctgacg ctgacctggt 1260
catatggaac cccaaggcca ccaagatcat ctctgccaa acccacaatc tgaacgtgga 1320
gtacaacatc ttcgaggag tggagtgccg gggagcgct gccgtggtca taagtcaggg 1380
ccgagtggcg ctggaggacg ggaagatggt tgtcaccccg ggggcgggccc gcttcgtccc 1440
tcggaaaaca ttcccgact ttgtctacaa gaggatcaaa gctcgcaaca ggctggcgga 1500
gatccacggt gtgccccgtg ggctgtatga cgggcccgtc cagaggtga tggtgctgc 1560
caagccaggg agtggcgctc cggcccgcg gtctgccca ggcaagatct ccgtgcctcc 1620
tgtgcgaac ctacatcagt cggggttcag cctatctggg tctcaggctg atgaccacat 1680
cgcccgcgc 1690

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<210> 8
<211> 572
<212> PRT
<213> Homo sapiens

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<400> 8
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Met Ser Phe Gln Gly Lys Lys Ser Ile Pro Arg Ile Thr Ser Asp Arg
1          5          10          15

```

```

Leu Leu Ile Arg Gly Gly Arg Ile Val Asn Asp Asp Gln Ser Phe Tyr
          20          25          30

```

```

Ala Asp Val His Val Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
          35          40          45

```

```

Leu Ile Val Pro Gly Gly Ile Lys Thr Ile Asp Ala His Gly Leu Met
          50          55          60

```

```

Val Leu Pro Gly Gly Val Asp Val His Thr Arg Leu Gln Met Pro Val
65          70          75          80

```

```

Leu Gly Met Thr Pro Ala Asp Asp Phe Cys Gln Gly Thr Lys Ala Ala
          85          90          95

```

Leu Ala Gly Gly Thr Thr Met Ile Leu Asp His Val Phe Pro Asp Thr
100 105 110

Gly Val Ser Leu Leu Ala Ala Tyr Glu Gln Trp Arg Glu Arg Ala Asp
115 120 125

Ser Ala Ala Cys Cys Asp Tyr Ser Leu His Val Asp Ile Thr Arg Trp
130 135 140

His Glu Ser Ile Lys Glu Glu Leu Glu Ala Leu Val Lys Glu Lys Gly
145 150 155 160

Val Asn Ser Phe Leu Val Phe Met Ala Tyr Lys Asp Arg Cys Gln Cys
165 170 175

Ser Asp Ser Gln Met Tyr Glu Ile Phe Ser Ile Ile Arg Asp Leu Gly
180 185 190

Ala Leu Ala Gln Val His Ala Glu Asn Gly Asp Ile Val Glu Glu Glu
195 200 205

Gln Lys Arg Leu Leu Glu Leu Gly Ile Thr Gly Pro Glu Gly His Val
210 215 220

Leu Ser His Pro Glu Glu Val Glu Ala Glu Ala Val Tyr Arg Ala Val
225 230 235 240

Thr Ile Ala Lys Gln Ala Asn Cys Pro Leu Tyr Val Thr Lys Val Met
245 250 255

Ser Lys Gly Ala Ala Asp Ala Ile Ala Gln Ala Lys Arg Arg Gly Val
260 265 270

Val Val Phe Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser
275 280 285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser
290 295 300

Pro Pro Val Asn Pro Asp Pro Thr Thr Ala Asp His Leu Thr Cys Leu
305 310 315 320

Leu Ser Ser Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe

	325		330		335												
Thr	Thr	Ala	Gln	Lys	Ala	Val	Gly	Lys	Asp	Asn	Phe	Ala	Leu	Ile	Pro		
	340							345					350				
Glu	Gly	Thr	Asn	Gly	Ile	Glu	Glu	Arg	Met	Ser	Met	Val	Trp	Glu	Lys		
	355						360					365					
Cys	Val	Ala	Ser	Gly	Lys	Met	Asp	Glu	Asn	Glu	Phe	Val	Ala	Val	Thr		
	370					375					380						
Ser	Thr	Asn	Ala	Ala	Lys	Ile	Phe	Asn	Phe	Tyr	Pro	Arg	Lys	Gly	Arg		
385					390					395					400		
Val	Ala	Val	Gly	Ser	Asp	Ala	Asp	Leu	Val	Ile	Trp	Asn	Pro	Lys	Ala		
			405						410					415			
Thr	Lys	Ile	Ile	Ser	Ala	Lys	Thr	His	Asn	Leu	Asn	Val	Glu	Tyr	Asn		
		420						425					430				
Ile	Phe	Glu	Gly	Val	Glu	Cys	Arg	Gly	Ala	Pro	Ala	Val	Val	Ile	Ser		
	435						440					445					
Gln	Gly	Arg	Val	Ala	Leu	Glu	Asp	Gly	Lys	Met	Phe	Val	Thr	Pro	Gly		
	450					455					460						
Ala	Gly	Arg	Phe	Val	Pro	Arg	Lys	Thr	Phe	Pro	Asp	Phe	Val	Tyr	Lys		
465					470					475					480		
Arg	Ile	Lys	Ala	Arg	Asn	Arg	Leu	Ala	Glu	Ile	His	Gly	Val	Pro	Arg		
				485					490					495			
Gly	Leu	Tyr	Asp	Gly	Pro	Val	His	Glu	Val	Met	Val	Pro	Ala	Lys	Pro		
			500					505					510				
Gly	Ser	Gly	Ala	Pro	Ala	Arg	Ala	Ser	Cys	Pro	Gly	Lys	Ile	Ser	Val		
		515					520					525					
Pro	Pro	Val	Arg	Asn	Leu	His	Gln	Ser	Gly	Phe	Ser	Leu	Ser	Gly	Ser		
	530					535					540						
Gln	Ala	Asp	Asp	His	Ile	Ala	Arg	Arg	Thr	Ala	Gln	Lys	Ile	Met	Ala		
545					550					555					560		

Pro Pro Gly Gly Arg Ser Asn Ile Thr Ser Leu Ser
565 570

<210> 9
<211> 55
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(55)
<223> amino acids 1 to 55 of the sequence shown in Figure 12

<400> 9

Met Ser Phe Gln Gly Lys Lys Ser Ile Pro Arg Ile Thr Ser Asp Arg
1 5 10 15

Leu Leu Ile Arg Gly Gly Arg Ile Val Asn Asp Asp Gln Ser Phe Tyr
20 25 30

Ala Asp Val His Val Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
35 40 45

Leu Ile Val Pro Gly Gly Ile
50 55

<210> 10
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(516)
<223> amino acids 57 to 553 of the sequence shown in Figure 12

<400> 10

Thr Ile Asp Ala His Gly Leu Met Val Leu Pro Gly Gly Val Asp Val
1 5 10 15

His Thr Arg Leu Gln Met Pro Val Leu Gly Met Thr Pro Ala Asp Asp
20 25 30

Phe Cys Gln Gly Thr Lys Ala Ala Leu Ala Gly Gly Thr Thr Met Ile
35 40 45
Leu Asp His Val Phe Pro Asp Thr Gly Val Ser Leu Leu Ala Ala Tyr
50 55 60
Glu Gln Trp Arg Glu Arg Ala Asp Ser Ala Ala Cys Cys Asp Tyr Ser
65 70 75 80
Leu His Val Asp Ile Thr Arg Trp His Glu Ser Ile Lys Glu Glu Leu
85 90 95
Glu Ala Leu Val Lys Glu Lys Gly Val Asn Ser Phe Leu Val Phe Met
100 105 110
Ala Tyr Lys Asp Arg Cys Gln Cys Ser Asp Ser Gln Met Tyr Glu Ile
115 120 125
Phe Ser Ile Ile Arg Asp Leu Gly Ala Leu Ala Gln Val His Ala Glu
130 135 140
Asn Gly Asp Ile Val Glu Glu Glu Gln Lys Arg Leu Leu Glu Leu Gly
145 150 155 160
Ile Thr Gly Pro Glu Gly His Val Leu Ser His Pro Glu Glu Val Glu
165 170 175
Ala Glu Ala Val Tyr Arg Ala Val Thr Ile Ala Lys Gln Ala Asn Cys
180 185 190
Pro Leu Tyr Val Thr Lys Val Met Ser Lys Gly Ala Ala Asp Ala Ile
195 200 205
Ala Gln Ala Lys Arg Arg Gly Val Val Val Phe Gly Glu Pro Ile Thr
210 215 220
Ala Ser Leu Gly Thr Asp Gly Ser His Tyr Trp Ser Lys Asn Trp Ala
225 230 235 240
Lys Ala Ala Ala Phe Val Thr Ser Pro Pro Val Asn Pro Asp Pro Thr
245 250 255

Thr Ala Asp His Leu Thr Cys Leu Leu Ser Ser Gly Asp Leu Gln Val
260 265 270

Thr Gly Ser Ala His Cys Thr Phe Thr Thr Ala Gln Lys Ala Val Gly
275 280 285

Lys Asp Asn Phe Ala Leu Ile Pro Glu Gly Thr Asn Gly Ile Glu Glu
290 295 300

Arg Met Ser Met Val Trp Glu Lys Cys Val Ala Ser Gly Lys Met Asp
305 310 315 320

Glu Asn Glu Phe Val Ala Val Thr Ser Thr Asn Ala Ala Lys Ile Phe
325 330 335

Asn Phe Tyr Pro Arg Lys Gly Arg Val Ala Val Gly Ser Asp Ala Asp
340 345 350

Leu Val Ile Trp Asn Pro Lys Ala Thr Lys Ile Ile Ser Ala Lys Thr
355 360 365

His Asn Leu Asn Val Glu Tyr Asn Ile Phe Glu Gly Val Glu Cys Arg
370 375 380

Gly Ala Pro Ala Val Val Ile Ser Gln Gly Arg Val Ala Leu Glu Asp
385 390 395 400

Gly Lys Met Phe Val Thr Pro Gly Ala Gly Arg Phe Val Pro Arg Lys
405 410 415

Thr Phe Pro Asp Phe Val Tyr Lys Arg Ile Lys Ala Arg Asn Arg Leu
420 425 430

Ala Glu Ile His Gly Val Pro Arg Gly Leu Tyr Asp Gly Pro Val His
435 440 445

Glu Val Met Val Pro Ala Lys Pro Gly Ser Gly Ala Pro Ala Arg Ala
450 455 460

Ser Cys Pro Gly Lys Ile Ser Val Pro Pro Val Arg Asn Leu His Gln
465 470 475 480

Ser Gly Phe Ser Leu Ser Gly Ser Gln Ala Asp Asp His Ile Ala Arg

485

490

495

Arg

<210> 11
<211> 6
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa corresponds to a non-determined amino acid

<400> 11

Xaa Met Tyr Asp Gly Pro
1 5

<210> 12
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa corresponds to a non-determined amino acid

<400> 12

Xaa Phe Asn Leu Tyr Pro Arg
1 5

<210> 13
<211> 13
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa corresponds to a non-determined amino acid

<400> 13

Xaa Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly
1 5 10

<210> 14
<211> 20
<212> PRT
<213> Mus musculus

<220>
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<223> Xaa corresponds to a non-determined amino acid

<220>
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<222> (4)..(5)
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<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa corresponds to a probable but uncertain His residue

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa corresponds to a non-determined amino acid

<400> 14

Xaa Ile Gly Xaa Xaa Ala Gln Val Xaa Ala Glu Asn Gly Xaa Ile Ile
1 5 10 15

Ala Glu Glu Gln
20

<210> 15
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> Xaa corresponds to a non-determined amino acid

<400> 15

Xaa Xaa Glu Asn Gln Phe Val Ala Val Thr
1 5 10

<210> 16
<211> 19

<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa corresponds to a non-determined amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa corresponds to a probably but non-determined Asp amino acid residue

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa corresponds to a probably but non-determined Asp amino acid residue

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa corresponds to a probably but non-determined Gly amino acid residue

<400> 16

Xaa	Val	Asn	Asp	Xaa	Gln	Ser	Phe	Tyr	Ala	Asp	Ile	Tyr	Met	Glu	Xaa
1				5					10					15	

Xaa Leu Ile

<210> 17
<211> 12
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> Xaa corresponds to a non-determined amino acid

<220>
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<222> (7)..(7)
<223> Xaa corresponds to a non-determined amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa corresponds to a non-determined amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa corresponds to a non-determined amino acid

<400> 17

Xaa Xaa Xaa Phe Val Thr Xaa Pro Xaa Leu Xaa Pro
1 5 10

<210> 18
<211> 6
<212> PRT
<213> Mus musculus

<400> 18

Ile Ile Ala Glu Glu Gln
1 5

<210> 19
<211> 8
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa corresponds to a probably but uncertain Asp amino acid
residue

<400> 19

Tyr Ala Asp Ile Tyr Met Glu Xaa
1 5

<210> 20
<211> 14
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide probe sequence

<220>
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<222> (3)..(3)
<223> n corresponds to either C or T

<220>
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<222> (9)..(9)
<223> n corresponds to either T or A

<220>
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<222> (12)..(12)
<223> n corresponds to either A or G

<400> 20
atnattgcng anca

14

<210> 21
<211> 16
<212> DNA
<213> Artificial

<220>
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<220>
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<223> n corresponds to either C or T

<220>
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<222> (6)..(6)
<223> n corresponds to either T or C

<220>
<221> misc_feature
<222> (9)..(9)
<223> n corresponds to either T or A

<220>
<221> misc_feature
<222> (14)..(14)
<223> n corresponds to either A or G

<400> 21
tgntcnacng catnat

16

<210> 22
<211> 17
<212> DNA
<213> Artificial

<220>
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<220>
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<222> (6)..(6)

<223> n corresponds to either A or T

<220>

<221> misc_feature

<222> (9)..(9)

<223> n corresponds to either C or T

<220>

<221> misc_feature

<222> (12)..(12)

<223> n corresponds to either C or T

<400> 22

tatgcngana tnatgga

17

<210> 23

<211> 17

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide probe

<220>

<221> misc_feature

<222> (6)..(6)

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<220>

<221> misc_feature

<222> (9)..(9)

<223> n corresponds to either G or A

<220>

<221> misc_feature

<222> (12)..(12)

<223> n corresponds to either T or A

<400> 23

tcctatntanc tngcata

17

<210> 24

<211> 23

<212> DNA

<213> Artificial

<220>

<223> primer sequence

<400> 24

ggcatatgtc ttatcagggg aag

23

<210> 25

<211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> primer sequence

 <400> 25
 gcgaattctt agcccaggct gatg 24

<210> 26
 <211> 12
 <212> PRT
 <213> Artificial

 <220>
 <223> artificial peptide antigen

 <400> 26

Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly Ser
 1 5 10

<210> 27
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> polynucleotide sequence

<220>
 <221> misc_feature
 <222> (1)..(28)
 <223> polynucleotide sequence between restrictions sites EcoRI and BamHI

 <400> 27
 atggactaca aggacgacga tgacaagg 28

<210> 28
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide probe

<400> 28
 atagaggagc ggatgacg 18

<210> 29

<211> 25
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide probe

 <400> 29
 gctggttatgg tcttcaactt gtcgg 25

<210> 30
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide probe

 <400> 30
 ggcctgttat ggtcttcaac ttgtcg 26

<210> 31
 <211> 20
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 <220>
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 <400> 31
 aggaggagtg aagaccatcg 20

<210> 32
 <211> 22
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 <220>
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 <400> 32
 cttatgccac tcgctgatgt cc 22

<210> 33
 <211> 19
 <212> DNA
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 <220>
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 <400> 33
 catctggctg tcgctgcac 19

<210> 34
<211> 19
<212> DNA
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<220>
<223> primer sequence

<400> 34
gccgcccta ccagagacc

19

<210> 35
<211> 18
<212> DNA
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<220>
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<400> 35
ggagattcag tgtggtgg

18

<210> 36
<211> 20
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<220>
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<400> 36
ggctctccag aacatcatcc

20

<210> 37
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<220>
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<400> 37

Gly Ser Ala Arg Gly Ser Pro Thr Arg Pro Asn
1 5 10

<210> 38
<211> 12
<212> PRT
<213> Artificial

<220>

<223> artificial peptide sequence

<400> 38

Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala
1 5 10

<210> 39

<211> 11

<212> PRT

<213> Artificial

<220>

<223> artificial peptide sequence

<400> 39

Pro Ser Ala Lys Ser Ser Pro Ser Lys His Gln
1 5 10

<210> 40

<211> 11

<212> PRT

<213> Artificial

<220>

<223> artificial peptide sequence

<400> 40

Pro Ala Arg Ala Ser Cys Pro Gly Lys Ile Ser
1 5 10